

09866582

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/866,582A

DATE: 12/27/2002
 TIME: 14:17:42

Input Set : A:\07917-145001.txt
 Output Set: N:\CRF4\12272002\I866582A.raw

4 <110> APPLICANT: Witman, George B.
 5 . Pazour, Gregory J.
 6 Rosenbaum, Joel L.
 7 Cole, Douglas G.
 9 <120> TITLE OF INVENTION: INTRAFLAGELLAR TRANSPORT
 11 <130> FILE REFERENCE: 07917-145001
 13 <140> CURRENT APPLICATION NUMBER: US 09/866,582A
 14 <141> CURRENT FILING DATE: 2001-05-24
 16 <150> PRIOR APPLICATION NUMBER: US 60/206,923
 17 <151> PRIOR FILING DATE: 2000-05-24
 19 <160> NUMBER OF SEQ ID NOS: 50
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 877
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Chlamydomonas reinhardtii
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (114)...(518)
 32 <400> SEQUENCE: 1
 33 caccgctgcc gctgaacaga aagtctgcgc agactcgctc tcttgccaaag ttcttgccaa 60
 34 aaccaggcagg cctagagggtt gccttaacct aaatatacaa aacacagagc atc atg 116
 35 Met
 36 1
 38 gac gcg gta gat aga gga gtc tac ttt gac gag gac ttt cat gtc cgc 164
 39 Asp Ala Val Asp Arg Gly Val Tyr Phe Asp Glu Asp Phe His Val Arg
 40 5 10 15
 42 att ctt gat gtt gac aag tac aat gct tca aag tcg ctc cag gag aac 212
 43 Ile Leu Asp Val Asp Lys Tyr Asn Ala Ser Lys Ser Leu Gln Asp Asn
 44 20 25 30
 46 aca aat gtg ttc att aac aac atc caa aat atg caa ggc ctc gtg gag 260
 47 Thr Asn Val Phe Ile Asn Asn Ile Gln Asn Met Gln Gly Leu Val Asp
 48 35 40 45
 50 aag tac gtg tcc gcc atc gac cag cag gtc gag cgg cta gaa gct gaa 308
 51 Lys Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg Leu Glu Ala Glu
 52 50 55 60 65
 54 aag ctg aag gcc att ggc ctg cgg aac cgg gtg gct gcg ctg agc gag 356
 55 Lys. Leu Lys Ala Ile Gly Leu Arg Asn Arg Val Ala Ala Leu Ser Glu
 56 70 75 80
 58 gag cgg aaa cgt aaa caa aag gag cag gag cgc atg cta gcg gag aag 404
 59 Glu Arg Lys Arg Lys Gln Lys Glu Gln Glu Arg Met Leu Ala Glu Lys
 60 85 90 95
 62 cag gag gag ctt gag agg ctc caa atg gag gag cag tcg ctg atc aag 452

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P.6

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Input Set : A:\07917-145001.txt
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63 Gln Glu Glu Leu Glu Arg Leu Gln Met Glu Glu Gln Ser Leu Ile Lys		
64 100 105 110		
66 gtg aag ggc gag cag gag ctc atg att cag aag ctg tcg gac agc agc	500	
67 Val Lys Gly Glu Gln Glu Leu Met Ile Gln Lys Leu Ser Asp Ser Ser		
68 115 120 125		
70 agc ggg gcg gca tac gtg taaacggtgt tcggacgtca tgcgtgcaaa	548	
71 Ser Gly Ala Ala Tyr Val		
72 130 135		
74 ggtagttgc tctgtgaggg ttggctgagg cggccggaggc tgctattgag gctgcagcat	608	
75 gccgtctggc ggcagatgtc cataacggta tgggggttg gcgcacagaac gaaacggcga	668	
76 ggggtgcgcaaa atgtcgtgca gaagcgcacgc tacagcatcc atggtacgta gaggcttact	728	
77 ggggtgtcagt gcgtcgccg ccactgggca cacacttgca gcgcaggagcg ccattgttg	788	
78 gcccacggat tgcgtcaagg acttgaacgg cgccagtgaa ggccgggaaat ggaatgtaaa	848	
79 caaacgactc gaaaaaaaaaaaaaaa	877	
81 <210> SEQ ID NO: 2		
82 <211> LENGTH: 135		
83 <212> TYPE: PRT		
84 <213> ORGANISM: Chlamydomonas reinhardtii		
86 <400> SEQUENCE: 2		
87 Met Asp Ala Val Asp Arg Gly Val Tyr Phe Asp Glu Asp Phe His Val		
88 1 5 10 15		
89 Arg Ile Leu Asp Val Asp Lys Tyr Asn Ala Ser Lys Ser Leu Gln Asp		
90 20 25 30		
91 Asn Thr Asn Val Phe Ile Asn Asn Ile Gln Asn Met Gln Gly Leu Val		
92 35 40 45		
93 Asp Lys Tyr Val Ser Ala Ile Asp Gln Gln Val Glu Arg Leu Glu Ala		
94 50 55 60		
95 Glu Lys Leu Lys Ala Ile Gly Leu Arg Asn Arg Val Ala Ala Leu Ser		
96 65 70 75 80		
97 Glu Glu Arg Lys Arg Lys Gln Lys Glu Gln Glu Arg Met Leu Ala Glu		
98 85 90 95		
99 Lys Gln Glu Glu Leu Glu Arg Leu Gln Met Glu Glu Gln Ser Leu Ile		
100 100 105 110		
101 Lys Val Lys Gly Glu Gln Glu Leu Met Ile Gln Lys Leu Ser Asp Ser		
102 115 120 125		
103 Ser Ser Gly Ala Ala Tyr Val		
104 130 135		
106 <210> SEQ ID NO: 3		
107 <211> LENGTH: 615		
108 <212> TYPE: DNA		
109 <213> ORGANISM: Chlamydomonas reinhardtii		
111 <220> FEATURE:		
112 <221> NAME/KEY: CDS		
113 <222> LOCATION: (1)...(612)		
115 <400> SEQUENCE: 3		
116 atg gtg aag aaa gaa gtg aag ccc atc gat atc acc gca acg cta aga	48	
117 Met Val Lys Lys Glu Val Lys Pro Ile Asp Ile Thr Ala Thr Leu Arg		
118 1 5 10 15		
120 tgc aaa gta gca gta gtc ggc gaa gcg act gtc ggc aag agc gcg ctc	96	

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Input Set : A:\07917-145001.txt
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121 Cys Lys Val Ala Val Val Gly Glu Ala Thr Val Gly Lys Ser Ala Leu			
122 20	25	30	
124 atc tct atg ttc acg agt aaa ggc agc aag ttt cta aag gac tat gcg			144
125 Ile Ser Met Phe Thr Ser Lys Gly Ser Lys Phe Leu Lys Asp Tyr Ala			
126 35	40	45	
128 atg acg agt ggg gtg gag gtg gtg gta gcc ccg gtg acc att ccg gac			192
129 Met Thr Ser Gly Val Glu Val Val Ala Pro Val Thr Ile Pro Asp			
130 50	55	60	
132 acg acg gtc tcg gtg gag ctc ttt ctg ctg gac acg gcg ggg agc gac			240
133 Thr Thr Val Ser Val Glu Leu Phe Leu Leu Asp Thr Ala Gly Ser Asp			
134 65	70	75	80
136 ctg tac aag gag cag ata tcg cag tac tgg aac ggc gta tac tac gcc			288
137 Leu Tyr Lys Glu Gln Ile Ser Gln Tyr Trp Asn Gly Val Tyr Tyr Ala			
138 85	90	95	
140 att ctc gtg ttc gat gtg agc tct atg gag tcc gag tcg tgc aag			336
141 Ile Leu Val Phe Asp Val Ser Ser Met Glu Ser Phe Glu Ser Cys Lys			
142 100	105	110	
144 gcg tgg ttt gag ctg ctc aaa tcg gcg cgt ccc gac cgc gag cgg ccg			384
145 Ala Trp Phe Glu Leu Leu Lys Ser Ala Arg Pro Asp Arg Glu Arg Pro			
146 115	120	125	
148 ctg cgc gcc gtg ctg gtg gcg aac aag acg gac ctt ccg ccg cag cgg			432
149 Leu Arg Ala Val Leu Val Ala Asn Lys Thr Asp Leu Pro Pro Gln Arg			
150 130	135	140	
152 cac cag gtg cgg ctg gac atg gcg cag gac tgg gcc acc acc aac acc			480
153 His Gln Val Arg Leu Asp Met Ala Gln Asp Trp Ala Thr Thr Asn Thr			
154 145	150	155	160
156 ctc gac ttc ttc gac gtg tcc gcg aac ccg ccc ggc aag gac gcg gat			528
157 Leu Asp Phe Phe Asp Val Ser Ala Asn Pro Pro Gly Lys Asp Ala Asp			
158 165	170	175	
160 gcg ccg ttc ctg tcc atc gcc acc acc ttc tac cgc aac tac gag gac			576
161 Ala Pro Phe Leu Ser Ile Ala Thr Thr Phe Tyr Arg Asn Tyr Glu Asp			
162 180	185	190	
164 aag gtg gcg gcc ttc cag gac gct tgc cgc aac tac tga			615
165 Lys Val Ala Ala Phe Gln Asp Ala Cys Arg Asn Tyr			
166 195	200		
168 <210> SEQ ID NO: 4			
169 <211> LENGTH: 204			
170 <212> TYPE: PRT			
171 <213> ORGANISM: Chlamydomonas reinhardtii			
173 <400> SEQUENCE: 4			
174 Met Val Lys Lys Glu Val Lys Pro Ile Asp Ile Thr Ala Thr Leu Arg			
175 1 5 10 15			
176 Cys Lys Val Ala Val Val Gly Glu Ala Thr Val Gly Lys Ser Ala Leu			
177 20 25 30			
178 Ile Ser Met Phe Thr Ser Lys Gly Ser Lys Phe Leu Lys Asp Tyr Ala			
179 35 40 45			
180 Met Thr Ser Gly Val Glu Val Val Ala Pro Val Thr Ile Pro Asp			
181 50 55 60			
182 Thr Thr Val Ser Val Glu Leu Phe Leu Asp Thr Ala Gly Ser Asp			

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183	65	70	75	80													
184	Leu	Tyr	Lys	Glu	Gln	Ile	Ser	Gln	Tyr	Trp	Asn	Gly	Val	Tyr	Tyr	Ala	
185																95	
186	Ile	Leu	Val	Phe	Asp	Val	Ser	Ser	Met	Glu	Ser	Phe	Glu	Ser	Cys	Lys	
187																110	
188	Ala	Trp	Phe	Glu	Leu	Leu	Lys	Ser	Ala	Arg	Pro	Asp	Arg	Glu	Arg	Pro	
189																125	
190	Leu	Arg	Ala	Val	Leu	Val	Ala	Asn	Lys	Thr	Asp	Leu	Pro	Pro	Gln	Arg	
191																140	
192	His	Gln	Val	Arg	Leu	Asp	Met	Ala	Gln	Asp	Trp	Ala	Thr	Thr	Asn	Thr	
193	145															160	
194	Leu	Asp	Phe	Phe	Asp	Val	Ser	Ala	Asn	Pro	Pro	Gly	Lys	Asp	Ala	Asp	
195																175	
196	Ala	Pro	Phe	Leu	Ser	Ile	Ala	Thr	Thr	Phe	Tyr	Arg	Asn	Tyr	Glu	Asp	
197																190	
198	Lys	Val	Ala	Ala	Phe	Gln	Asp	Ala	Cys	Arg	Asn	Tyr					
199																200	
201	<210>	SEQ	ID	NO:	5												
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203	<212>	TYPE:	DNA														
204	<213>	ORGANISM:	Chlamydomonas reinhardtii														
206	<220>	FEATURE:															
207	<221>	NAME/KEY:	CDS														
208	<222>	LOCATION:	(1)...(1032)														
210	<400>	SEQUENCE:	5														
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212	Met	Asp	Asp	Ser	Met	Asp	Tyr	Pro	Asp	Arg	Asp	Gly	Asp	Asp	Leu	Asp	
213	1				5				10						15		
215	cag	ttc	cag	ggc	acc	gcg	cgc	tcg	cag	gtc	gtg	cag	aac	cag	ccg	cac	96
216	Gln	Phe	Gln	Gly	Thr	Ala	Arg	Ser	Gln	Val	Val	Gln	Asn	Gln	Pro	His	
217																30	
219	gac	gag	gag	gtg	aat	ctg	agt	gag	tcg	gag	agc	ttc	gcg	gga	gcf	gat	144
220	Asp	Glu	Glu	Val	Asn	Leu	Ser	Glu	Ser	Glu	Ser	Phe	Ala	Gly	Ala	Asp	
221																45	
223	gag	cct	cca	gct	gct	cca	gca	gat	gct	tcg	ctc	ata	gag	tca	cac	gac	192
224	Glu	Pro	Pro	Ala	Ala	Pro	Arg	Asp	Ala	Ser	Leu	Ile	Glu	Ser	His	Asp	
225																60	
229	atg	gac	gag	ggg	cca	gct	gct	cca	gca	cg	aca	ctc	tca	cca	acg	ggc	240
230	Met	Asp	Glu	Gly	Pro	Ala	Ala	Pro	Ala	Arg	Thr	Leu	Ser	Pro	Thr	Gly	
231	65															80	
233	tat	gag	gct	gga	aag	cac	gca	cct	ggc	ggc	atc	gcc	aac	tcg	gac	gag	288
234	Tyr	Glu	Ala	Gly	Lys	His	Ala	Pro	Gly	Gly	Ile	Ala	Asn	Ser	Asp	Glu	
235																95	
237	gca	ccg	ccg	ggt	gct	tac	aac	gca	cag	gag	tac	aag	cac	ctg	aac	gtg	336
238	Ala	Pro	Pro	Gly	Ala	Tyr	Asn	Ala	Gln	Glu	Tyr	Lys	His	Leu	Asn	Val	
239																110	
241	ggc	gag	gac	gtg	cgc	gag	ctg	ttc	tcc	tac	atc	ggc	cgc	tac	aag	ccg	384
242	Gly	Glu	Asp	Val	Arg	Glu	Leu	Phe	Ser	Tyr	Ile	Gly	Arg	Tyr	Lys	Pro	
243																125	

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Input Set : A:\07917-145001.txt
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245 cag acg gtg gag ctg gac acg cgc atc aag ccc ttc atc cct gac tac	432
246 Gln Thr Val Glu Leu Asp Thr Arg Ile Lys Pro Phe Ile Pro Asp Tyr	
247 130 135 140	
249 atc ccc gcg gtg ggc ggc atc gac gag ttc atc aag gtg ccg cga ccc	480
250 Ile Pro Ala Val Gly Gly Ile Asp Glu Phe Ile Lys Val Pro Arg Pro	
251 145 150 155 160	
253 gac acc aag ccc gac tac ctg ggg ctc aag gtt ctg gac gag ccg gcc	528
254 Asp Thr Lys Pro Asp Tyr Leu Gly Leu Lys Val Leu Asp Glu Pro Ala	
255 165 170 175	
257 gcc aag cag tcg gac ccc acg gtg ctg acg ctg cag ctg cgg cag ctg	576
258 Ala Lys Gln Ser Asp Pro Thr Val Leu Thr Leu Gln Leu Arg Gln Leu	
259 180 185 190	
261 tcc aag gag gcg ccg ggc gcc aag gcc gac atg gtg ggg cgg ctg gag	624
262 Ser Lys Glu Ala Pro Gly Ala Lys Ala Asp Met Val Gly Arg Leu Glu	
263 195 200 205	
265 cac acc gac gag aac aag gcc aag aag atc cag cag tgg atc gcc tcc	672
266 His Thr Asp Glu Asn Lys Ala Lys Lys Ile Gln Gln Trp Ile Ala Ser	
267 210 215 220	
269 atc aac gac atc cac aag gcc aag ccg gcc acc gtc aac tac agc	720
270 Ile Asn Asp Ile His Lys Ala Lys Pro Ala Ala Thr Val Asn Tyr Ser	
271 225 230 235 240	
273 aag cgc atg cca gag atc gag gcg ctg atg cag gag tgg ccg ccg gag	768
274 Lys Arg Met Pro Glu Ile Glu Ala Leu Met Gln Glu Trp Pro Pro Glu	
275 245 250 255	
277 gtg gag acc ttc ctc aag acc atg cac atg ccg tcc ggc gat gtg gag	816
278 Val Glu Thr Phe Leu Lys Thr Met His Met Pro Ser Gly Asp Val Glu	
279 260 265 270	
281 ctg gac atc aag acc tac gcc ccg ctg gtg tgc acg ctg ctg gac att	864
282 Leu Asp Ile Lys Thr Tyr Ala Arg Leu Val Cys Thr Leu Leu Asp Ile	
283 275 280 285	
286 ccc gtg tac gac gac ccc gtg gag agc ctg cac gtg ctg ttc aca ctg	912
287 Pro Val Tyr Asp Asp Pro Val Glu Ser Leu His Val Leu Phe Thr Leu	
288 290 295 300	
290 tac ctg gag ttc aag aac aac ccc atc ttc agg cag cac atg gag atg	960
291 Tyr Leu Glu Phe Lys Asn Asn Pro Ile Phe Arg Gln His Met Glu Met	
292 305 310 315 320	
294 gag aac aag ctg gac ggc atg tcg ggc ggc ggc ggc atg atg ggc	1008
295 Glu Asn Lys Leu Asp Gly Met Ser Gly Gly Gly Gly Met Met Gly	
296 325 330 335	
298 ggc ggc gcg gat gtg ctg ggc ttg tga	1035
299 Gly Gly Ala Asp Val Leu Gly Leu	
300 340	
302 <210> SEQ ID NO: 6	
303 <211> LENGTH: 344	
304 <212> TYPE: PRT	
305 <213> ORGANISM: Chlamydomonas reinhardtii	
307 <400> SEQUENCE: 6	
308 Met Asp Asp Ser Met Asp Tyr Pro Asp Arg Asp Gly Asp Asp Leu Asp	
309 1 5 10 15	

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/866,582A

DATE: 12/27/2002
TIME: 14:17:43

Input Set : A:\07917-145001.txt
Output Set: N:\CRF4\12272002\I866582A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:21; Xaa Pos. 698
Seq#:22; Xaa Pos. 698
Seq#:24; Xaa Pos. 24
Seq#:25; Xaa Pos. 66